

AMENDMENTS TO THE SPECIFICATION

Please add the following new paragraph at page 3, line 28:

The invention also provides a purified protein comprising a fragment of a Nogo protein comprising an amino acid sequence selected from the group consisting of residues 31-57 depicted in Figure 2a (SEQ ID NO:2), residues 11-191 depicted in Figure 14 (SEQ ID NO:32), residues 988-1023 depicted in Figure 2a (SEQ ID NO:2), residues 1090-1125 depicted in Figure 2a (SEQ ID NO:2), residues 994-1174 depicted in Figure 13 (SEQ ID NO:29), residues 977-1012 depicted in Figure 13 (SEQ ID NO:29), and residues 1079-1114 depicted in Figure 13 (SEQ ID NO:29).

Please replace the paragraph on page 5 beginning with "Figure 2a-2b" with the following paragraph:

Figure ~~2a-2b~~: (a) 2A1 to 2A4: Nucleotide (SEQ ID NO:1) and amino acid sequences (SEQ ID NO:2) of *Nogo* transcript A (sequence generated by connecting RO18U37-3, Oli18, and R1-3U21 cDNA sequences). Oval box: presumed initiation codon; underlined with dots: acidic stretch; □: potential PKC sites; Δ: potential casein kinase II sites; thick underline: carboxy terminal hydrophobic regions and potential transmembrane domains; thin underline: potential N-glycosylation sites. [(b)] 2B: Peptide sequence comparison between sequenced, purified bovine NI220 (bNI220; SEQ ID NOS:3-8), and the corresponding bovine (SEQ ID NOS:9-14) and rat (SEQ ID NOS:15-20) sequences translated from rat and bovine cDNAs. Rat and bovine amino acid sequences, which do not match the bNI220 peptide sequences, are in lower case.

Please replace the paragraph on page 8 beginning with "Figure 12" with the following paragraph:

Figure [12:] 12A to 12D: The nucleotide sequence (SEQ ID NO:28) of the bovine *Nogo* cDNA.

Please replace the paragraph on page 8 beginning with "Figure 13" with the following paragraph:

Figure [13:] 13A-13B: The amino acid sequence of rat Nogo A (SEQ ID NO:2) aligned with the theoretical amino acid sequence of human Nogo (SEQ ID NO:29). The human Nogo amino acid sequence was derived from aligning expressed sequence tags (EST) to the rat Nogo sequence and translating the aligned human ESTs using the rat Nogo as a guiding template.

Please replace the paragraph on page 8 beginning with "Figure 14" with the following paragraph:

Figure [14:] 14A-14C: Rat Nogo C nucleic acid (SEQ ID NO:31) sequence and its corresponding amino acid sequence (SEQ ID NO:32).

Please replace the paragraph on page 16 beginning with "By way of example" with the following paragraph:

By way of example and not limitation, useful computer homology programs include the following: Basic Local Alignment Search Tool (BLAST) (~~www.ncbi.nlm.nih.gov~~ home page of the National Center for Biotechnology Information) (Altschul et al., 1990, J. of Molec. Biol., 215:403-410, "The BLAST Algorithm; Altschul et al., 1997, Nuc. Acids Res. 25:3389-3402) a heuristic search algorithm tailored to searching for sequence similarity which ascribes significance using the statistical methods of Karlin and Altschul 1990, Proc. Nat'l Acad. Sci. USA, 87:2264-68; 1993, Proc. Nat'l Acad. Sci. USA 90:5873-77. Five specific BLAST programs perform the following tasks:

- 1) The BLASTP program compares an amino acid query sequence against a protein sequence database.
- 2) The BLASTN program compares a nucleotide query sequence against a nucleotide sequence database.
- 3) The BLASTX program compares the six-frame conceptual translation products of a nucleotide query sequence (both strands) against a protein sequence database.

4) The TBLASTN program compares a protein query sequence against a nucleotide sequence database translated in all six reading frames (both strands).

5) The TBLASTX program compares the six-frame translations of a nucleotide query sequence against the six-frame translations of a nucleotide sequence database.

Please replace the paragraph on page 16 beginning with "Smith-Waterman" with the following paragraph:

Smith-Waterman (database: European Bioinformatics Institute ~~wwwz.ebi.ac.uk/bic_sw/~~) (Smith-Waterman, 1981, J. of Molec. Biol., 147:195-197) is a mathematically rigorous algorithm for sequence alignments.

Please replace the paragraph on page 16 beginning with "FASTA" with the following paragraph:

FASTA (see Pearson et al., 1988, Proc. Nat'l Acad. Sci. USA, 85:2444-2448) is a heuristic approximation to the Smith-Waterman algorithm. For a general discussion of the procedure and benefits of the BLAST, Smith-Waterman and FASTA algorithms, see Nicholas et al., 1998, "A Tutorial on Searching Sequence Databases and Sequence Scoring Methods" (~~www.psc.edu~~ home page of the Pittsburgh Supercomputing Center) and references cited therein.